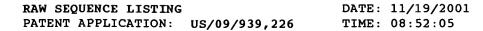0590
1209

#2   OIPE

RAW SEQUENCE LISTING   DATE: 11/19/2001
PATENT APPLICATION: US/09/939,226   TIME: 08:52:05

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Output Set: N:\CRF3\11192001\I939226.raw

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 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: SAMSON, MICHEL
 6                     PARMENTIER, MARC
 7                     VASSART, GILBERT
 8                     LIBERT, FREDERICK
10     (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
11                              AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
13    (iii) NUMBER OF SEQUENCES: 17
15·    (iv) CORRESPONDENCE ADDRESS:
16          (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
17          (B) STREET: 620 Newport Center Drive 16th Floor
18          (C) CITY: Newport Beach
19          (D) STATE: CA
20          (E) COUNTRY: U.S.A.
21          (F) ZIP: 92660
23     (v) COMPUTER READABLE FORM:
24          (A) MEDIUM TYPE: Floppy disk
25          (B) COMPUTER: IBM PC compatible
26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29     (vi) CURRENT APPLICATION DATA:
30          (A) APPLICATION NUMBER: US/09/939,226
31          (B)·FILING DATE: 24-Aug-2001
32          (C) CLASSIFICATION:
35    (vii) PRIOR APPLICATION DATA:
36          (A) APPLICATION NUMBER: 09/626,939
37          (B) FILING DATE: 2000-07-27
42   (viii) ATTORNEY/AGENT INFORMATION:
43          (A)·NAME: Altman, Daniel E
44          (B) REGISTRATION NUMBER: 34,115
45          (C) REFERENCE/DOCKET NUMBER:
47 (2) INFORMATION FOR SEQ ID NO: 1:
49      (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 792 base pairs
51          (B) TYPE: nucleic acid
52          (C)·STRANDEDNESS: single
53          (D) TOPOLOGY: linear
55     (ii) MOLECULE TYPE: DNA (genomic)
58     (ix) FEATURE:
59          (A) NAME/KEY: CDS
60          (B) LOCATION: 240..791
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68 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG      239
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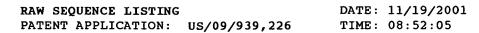
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RAW SEQUENCE LISTING   DATE: 11/19/2001
PATENT APPLICATION: US/09/939,226   TIME: 08:52:05

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73  Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
74          20                  25                  30
75  CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC    383
76  Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
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78  ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG    431
79  Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
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85  Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
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88  Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
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90  TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG    623
91  Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
92          115                 120                 125
93  GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT    671
94  Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
95          130                 135                 140
96  GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT    719
97  Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
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111         (B) TYPE: nucleic acid
112         (C) STRANDEDNESS: single
113         (D) TOPOLOGY: linear
115     (ii) MOLECULE TYPE: DNA (genomic)
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120         (B) LOCATION: 240..1295
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129 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA       287
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131  1                   5                  10                  15
132 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC       335
133 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
134             20                  25                  30
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142 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
143 65                  70                  75                  80
144 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT       527
145 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
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150 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG       623
151 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
152         115                 120                 125
153 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT       671
154 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
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156 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT       719
157 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
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PATENT APPLICATION: US/09/939,226   TIME: 08:52:05

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206         (C) STRANDEDNESS: single
207         (D) TOPOLOGY: linear
209     (ii) MOLECULE TYPE: DNA (genomic)
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213         (A) NAME/KEY: CDS
214         (B) LOCATION: 240..884
217     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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222 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG       239
223 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA       287
224 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
225   1                 5                 10                 15
226 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC       335
227 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
228             20                 25                 30
229 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC       383
230 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
231         35                 40                 45
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              PATENT APPLICATION:  US/09/939,226    TIME: 08:52:05

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236 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
237 65                    70                    75                    80
238 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT     527
239 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
240                    85                    90                    95
241 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC     575
242 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
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244 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG     623
245 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
246          115                   120                   125
247 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT     671
248 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
249      130                   135                   140
250 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT     719
251 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
252 145                   150                   155                   160
253 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC     767
254 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
255                    165                   170                   175
256 ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT     815
257 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
258          180                   185                   190
259 GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA     863
260 Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
261          195                   200                   205
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263 Asn Ser Ala Ser Val Ser Lys
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270 CTCAGTTTAC ACCCGATCCA CTGGGGAGCA GGAAATATCT GTGGGCTTGT GACACGGACT   1274
271 CAAGTGGGCT GGTGACCCAG TCAGAGTTGT GCACATGGCT TAGTTTTCAT ACACAGCCTG   1334
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279          (A) LENGTH: 184 amino acids
280          (B) TYPE: amino acid
281          (D) TOPOLOGY: linear
283      (ii) MOLECULE TYPE: protein
285      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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VERIFICATION SUMMARY DATE: 11/19/2001
PATENT APPLICATION: US/09/939,226 TIME: 08:52:06

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